

Title: 32544, A NOVEL HUMAN PHOSPHOLIPASE C AND
USES THEREOF

Inventors: Rachel Meyers et al.

Application No.: Not yet assigned

Docket No.: 381552004800

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TCGCGATCTAGAACTAGTGGCACGGCTCCTGCACTCCCACTGCCGAGGAACCTGCTCAGGAACCTGCCGGTCTCCGGCT	SEQ ID NO:1
GGGACGGTGGCTGGATCAGCTCAAGCCTCCAGGGCCCTGAGGCTGAGGGGCTGAGTGCTCATTCAGCCGCCTCGGGGA	
ACCCGGGCTGGGAGACCCCATGCCTGGGGGTGAGCCTGGAGCCAGGGCAGTGCGGTGAGAGGCTCCGGAGAGAGGGCTG	
GGCACCACCAGGCTTGGGTGTGTGATGCGCTGCTGGCCCAGGCTACACCCCGACAAGGGACACCGGGGGCCCTGGGAGC	
AGAGAGACCTCAGAGCAGCCTCCTCCTGCCTCCTGTGGACGGCCGCCCCAGCTGGTGATCCCAGCCAGTCCCAGCTTT	
CAGTTGCTGCCCCACCGACAGTCCCTCAGTCCCTCCATG	10 SEQ ID NO:2
ATG GCT CCC CCG ACA GCC GGC CCC CTT CCT	30
G P A L P P E D P G P D P E S R W L F L	30
GGC CCA GCT CTT CCG CCT GAG GAC CCA GGG CCG GAT CCG GAG AGC AGG TGG CTT TTC TTG	90
S A N I L P V V E R C M G A M Q E G M Q	50
AGC GCC AAC ATT CTG CCC GTG GTG GAG CGG TGC ATG GGT GCC ATG CAA GAG GGG ATG CAG	150
M V K L R G G S K G L V R F Y Y L D E H	70
ATG GTG AAG CTG CGT GGC GGC TCC AAG GGC CTG GTC CGC TTC TAC TAC CTG GAC GAG CAC	210
R S C I R W R P S R K N E K A K I S I D	90
CGC TCC TGC ATC CGC TGG AGG CCC TCA CGC AAG AAC GAG AAG GCC AAG ATC TCC ATC GAC	270
S I Q E V S E G R Q S E V F Q R Y P D G	110
TCC ATC CAG GAG GTG AGT GAG GGG CGG CAG TCG GAG GTC TTC CAG CGC TAC CCT GAC GGC	330
S F D P N C C F S I Y H G S H R E S L D	130
AGC TTC GAC CCC AAC TGC TGC TTC AGC ATC TAC CAC GGC AGC CAC CGC GAG TCG CTG GAC	390
L V S T S S E V A R T W V T G L R Y L M	150
CTG GTC TCC ACC AGC AGC GAG GTG GCG CGC ACC TGG GTC ACT GGC CTG CGC TAC CTC ATG	450
A G I S D E D S L A R R Q R T R D Q W L	170
GCC GGC ATC AGC GAC GAG GAC AGC CTG GCT CGC CGC CAG CGC ACC AGG GAC CAG TGG CTG	510
K Q T F D E A D K N G D G S L S I G E V	190
AAG CAG ACG TTT GAC GAG GCC GAC AAG AAC GGG GAT GGC AGC CTG AGC ATT GGC GAG GTC	570
L Q L L H K L N V N L P R Q R V K Q M F	210
CTG CAG CTG CTG CAC AAG CTC AAC GTG AAC CTG CCC CGG CAG AGG GTG AAG CAG ATG TTC	630
R E A D T D D H Q G T L G F E E F C A F	230
AGG GAA GCG GAC ACG GAT GAC CAC CAA GGG ACG CTG GGT TTT GAA GAG TTC TGT GCC TTC	690
Y K M M S T R R D L Y L L M L T Y S N H	250
TAC AAG ATG ATG TCC ACC CGC CGG GAC CTC TAC CTG CTC ATG CTG ACC TAC AGC AAC CAC	750
K D H L D A A S L Q R F L Q V E Q K M A	270
AAG GAC CAC CTG GAT GCC GCC AGC CTG CAG CGC TTC CTG CAG GTG GAG CAG AAG ATG GCG	810
G V T L E S C Q D I I E Q F E P C P E N	290
GGT GTG ACC CTC GAG AGC TGC CAG GAC ATC ATC GAG CAG TTT GAG CCA TGC CCA GAA AAC	870
K S K G L L G I D G F T N Y T R S P A G	310
AAG AGT AAG GGG CTG CTG GGC ATT GAT GGC TTC ACC AAC TAC ACC AGG AGC CCT GCT GGT	930
D I F N P E H H H V H Q D M T Q P L S H	330
GAC ATC TTC AAC CCT GAG CAC CAC CAT GTG CAC CAG GAC ATG ACG CAG CCG CTG AGC CAC	990
Y F I T S S H N T Y L V G D Q L M S Q S	350
TAC TTC ATC ACC TCG TCC CAC AAC ACC TAC CTC GTG GGT GAC CAG CTC ATG TCC CAG TCA	1050
R V D M Y A W V L Q A G C R C V E V D C	370
CGG GTG GAC ATG TAT GCT TGG GTC CTG CAG GCT GGC TGC CGC TGC GTG GAG GTG GAC TGC	1110
W D G P D G E P I V H H G Y T L T S K I	390
TGG GAT GGG CCC GAC GGG GAG CCC ATT GTG CAC CAT GGC TAC ACT CTG ACT TCC AAG ATC	1170

FIGURE 1a

L	F	K	D	V	I	E	T	I	N	K	Y	A	F	I	K	N	E	Y	P	410
CTC	TTC	AAA	GAC	GTC	ATT	GAA	ACC	ATC	AAC	AAA	TAT	GCC	TTC	ATC	AAG	AAT	GAG	TAC	CCA	1230
V	I	L	S	I	E	N	H	C	S	V	I	Q	Q	K	K	M	A	Q	Y	430
GTG	ATC	CTG	TCC	ATC	GAA	AAC	CAC	TGC	AGT	GTC	ATC	CAG	CAG	AAG	AAA	ATG	GCC	CAG	TAT	1290
L	T	D	I	L	G	D	K	L	D	L	S	S	V	S	S	E	D	A	T	450
CTG	ACT	GAC	ATC	CTT	GGG	GAC	AAG	CTG	GAC	CTG	TCA	TCA	GTG	AGC	AGT	GAA	GAT	GCC	ACC	1350
T	L	P	S	P	Q	M	L	K	G	K	I	L	V	K	G	K	K	L	P	470
ACA	CTC	CCC	TCT	CCA	CAG	ATG	CTC	AAG	GGC	AAG	ATC	CTC	GTG	AAG	GGG	AAG	AAG	CTC	CCA	1410
A	N	I	S	E	D	A	E	E	G	E	V	S	D	E	D	S	A	D	E	490
GCC	AAC	ATC	AGC	GAG	GAT	GCG	GAG	GAA	GGC	GAG	GTG	TCT	GAT	GAG	GAC	AGT	GCT	GAT	GAG	1470
I	D	D	D	C	K	L	L	N	G	D	A	S	T	N	R	K	R	V	E	510
ATT	GAC	GAT	GAC	TGC	AAG	CTC	CTC	AAT	GGG	GAT	GCA	TCC	ACC	AAT	CGA	AAG	CGT	GTA	GAA	1530
N	T	A	K	R	K	L	D	S	L	I	K	E	S	K	I	R	D	C	E	530
AAC	ACT	GCT	AAG	AGG	AAA	CTG	GAT	TCC	CTC	ATC	AAA	GAG	TCG	AAG	ATT	CGG	GAC	TGT	GAG	1590
D	P	N	N	F	S	V	S	T	L	S	P	S	G	K	L	G	R	K	S	550
GAC	CCC	AAC	AAC	TTC	TCC	GTC	TCC	ACA	CTG	TCC	CCA	TCT	GGA	AAG	CTC	GGA	CGC	AAG	AGC	1650
K	A	E	E	D	V	E	S	G	E	D	A	G	A	S	R	R	N	G	R	570
AAG	GCT	GAA	GAG	GAC	GTG	GAG	TCT	GGG	GAG	GAT	GCC	GGG	GCC	AGC	AGA	CGC	AAT	GGC	CGC	1710
L	V	V	G	S	F	S	R	R	K	K	K	G	S	K	L	K	K	A	A	590
CTC	GTC	GTG	GGA	AGC	TTC	TCC	AGG	CGC	AAG	AAG	AAG	GGC	AGC	AAG	CTG	AAG	AAG	GCG	GCC	1770
S	V	E	E	G	D	E	G	Q	D	S	P	G	G	Q	S	R	G	A	T	610
AGC	GTG	GAG	GAG	GGA	GAT	GAG	GGT	CAG	GAC	TCC	CCG	GGA	GGC	CAG	AGC	CGA	GGG	GCG	ACC	1830
R	Q	K	K	T	M	K	L	S	R	A	L	S	D	L	V	K	Y	T	K	630
CGG	CAG	AAG	AAG	ACC	ATG	AAG	CTG	TCC	CGG	GCC	CTC	TCT	GAC	CTG	GTG	AAG	TAC	ACC	AAG	1890
S	V	A	T	H	D	I	E	M	E	A	A	S	S	W	Q	V	S	S	F	650
TCC	GTG	GCC	ACC	CAC	GAC	ATA	GAG	ATG	GAG	GCG	GCG	TCC	AGC	TGG	CAG	GTG	TCG	TCC	TTC	1950
S	E	T	K	A	H	Q	I	L	Q	Q	K	P	A	Q	Y	L	R	F	N	670
AGC	GAG	ACC	AAG	GCC	CAC	CAG	ATT	CTG	CAG	CAG	AAG	CCG	GCG	CAG	TAC	CTA	CGC	TTC	AAC	2010
Q	Q	Q	L	S	R	I	Y	P	S	S	Y	R	V	D	S	S	N	Y	N	690
CAG	CAG	CAG	CTC	TCC	CGC	ATC	TAC	CCC	TCC	TCC	TAC	CGT	GTG	GAC	TCC	AGC	AAC	TAC	AAC	2070
P	Q	P	F	W	N	A	G	C	Q	M	V	A	L	N	Y	Q	S	E	G	710
CCG	CAG	CCC	TTC	TGG	AAC	GCC	GGC	TGC	CAA	ATG	GTT	GCC	CTG	AAC	TAC	CAG	TCA	GAG	GGG	2130
R	M	L	Q	L	N	R	A	K	F	S	A	N	G	G	C	G	Y	V	L	730
CGG	ATG	CTG	CAG	CTG	AAC	CGA	GCC	AAG	TTC	AGC	GCC	AAC	GGT	GGC	TGC	GGC	TAC	GTA	CTC	2190
K	P	G	C	M	C	Q	G	V	F	N	P	N	S	E	D	P	L	P	G	750
AAG	CCT	GGG	TGC	ATG	TGC	CAG	GGC	GTG	TTC	AAC	CCC	AAC	TCG	GAG	GAC	CCC	CTG	CCC	GGG	2250
Q	L	K	K	Q	L	V	L	R	I	I	S	G	Q	Q	L	P	K	P	R	770
CAG	CTC	AAG	AAG	CAG	CTG	GTG	CTC	CGG	ATC	ATC	AGT	GGC	CAG	CAG	CTT	CCC	AAG	CCG	CGC	2310
D	S	M	L	G	D	R	G	E	I	I	D	P	F	V	E	V	E	I	I	790
GAC	TCC	ATG	CTG	GGG	GAC	CGT	GGG	GAG	ATC	ATC	GAC	CCC	TTT	GTG	GAG	GTG	GAG	ATC	ATT	2370
G	L	P	V	D	C	S	R	E	Q	T	R	V	V	D	D	N	G	F	N	810
GGG	CTC	CCT	GTG	GAC	TGC	AGC	AGG	GAG	CAG	ACC	CGC	GTG	GTG	GAC	GAC	AAC	GGG	TTC	AAC	2430
P	T	W	E	E	T	L	V	F	M	V	H	M	P	E	I	A	L	V	R	830
CCC	ACC	TGG	GAG	GAG	ACC	CTG	GTT	TTC	ATG	GTG	CAC	ATG	CCG	GAG	ATC	GCG	CTG	GTC	CGC	2490
F	L	V	W	D	H	D	P	I	G	R	D	F	I	G	Q	R	T	L	A	850
TTC	CTC	GTC	TGG	GAC	CAC	GAT	CCC	ATC	GGG	CGT	GAC	TTC	ATT	GGC	CAG	AGG	ACG	CTG	GCC	2550
F	S	S	M	M	P	G	Y	R	H	V	Y	L	E	G	M	E	E	A	S	870
TTC	AGC	AGC	ATG	ATG	CCA	GGC	TAC	AGA	CAC	GTG	TAC	CTA	GAA	GGG	ATG	GAA	GAG	GCC	TCC	2610

FIGURE 1b

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I	F	V	H	V	A	V	S	D	I	S	G	K	V	K	Q	A	L	G	L	890
ATC	TTC	GTG	CAT	GTG	GCT	GTC	AGT	GAC	ATC	AGC	GGT	AAG	GTC	AAG	CAG	GCT	CTG	GGC	CTA	2670
K	G	L	F	L	R	G	P	K	P	G	S	L	D	S	H	A	A	G	R	910
AAA	GGC	CTC	TTC	CTC	CGA	GGC	CCA	AAG	CCC	GGC	TCG	CTG	GAC	AGT	CAT	GCT	GCT	GGG	CGG	2730
P	P	A	R	P	S	V	S	Q	R	I	L	R	R	T	A	S	A	P	T	930
CCC	CCG	GCC	CGG	CCC	TCC	GTT	AGC	CAG	CGG	ATC	CTG	CGG	CGC	ACG	GCC	AGC	GCC	CCG	ACC	2790
K	S	Q	K	P	G	R	R	G	F	P	E	L	V	L	G	T	R	D	T	950
AAG	AGC	CAG	AAG	CCG	GGC	CGC	AGG	GGC	TTC	CCG	GAG	CTG	GTC	CTG	GGT	ACA	CGG	GAC	ACA	2850
G	S	K	G	V	A	D	D	V	V	P	P	G	P	G	P	A	P	E	A	970
GGC	TCC	AAG	GGG	GTG	GCA	GAC	GAT	GTG	GTG	CCC	CCC	GGG	CCC	GGA	CCT	GCT	CCG	GAA	GCC	2910
P	A	Q	E	G	P	G	S	G	S	P	R	G	K	A	P	A	A	V	A	990
CCA	GCC	CAG	GAG	GGG	CCC	GGC	AGC	GGC	AGC	CCC	CGA	GGT	AAG	GCG	CCA	GCT	GCG	GTG	GCA	2970
E	K	S	P	V	R	V	R	P	P	R	V	L	D	G	P	G	P	A	G	1010
GAG	AAG	AGC	CCT	GTG	CGA	GTG	CGG	CCC	CCG	CGT	GTC	CTG	GAC	GGC	CCC	GGG	CCT	GCT	GGG	3030
M	A	A	T	C	M	K	C	V	V	G	S	C	A	G	V	N	T	G	G	1030
ATG	GCC	GCC	ACA	TGC	ATG	AAG	TGT	GTG	GTG	GGA	TCC	TGC	GCC	GGC	GTG	AAC	ACC	GGG	GGC	3090
L	Q	R	E	R	P	P	S	P	G	P	A	S	R	Q	A	A	I	R	Q	1050
CTG	CAG	AGG	GAG	CGG	CCA	CCC	AGC	CCG	GGG	CCT	GCA	AGC	AGG	CAG	GCA	GCC	ATT	CGC	CAG	3150
Q	P	R	A	R	A	D	S	L	G	A	P	C	C	G	L	D	P	H	A	1070
CAG	CCC	CGG	GCC	CGG	GCT	GAC	TCA	CTG	GGG	GCC	CCC	TGC	TGT	GGC	CTG	GAC	CCT	CAC	GCT	3210
I	P	G	R	S	R	E	A	P	K	G	P	G	A	W	R	Q	G	P	G	1090
ATC	CCG	GGG	AGA	AGC	AGA	GAG	GCC	CCC	AAG	GGT	CCT	GGG	GCC	TGG	AGG	CAG	GGT	CCA	GGC	3270
G	S	G	S	M	S	S	D	S	S	S	P	D	S	P	G	I	P	E	R	1110
GGT	AGC	GGC	TCC	ATG	TCC	TCG	GAC	TCC	AGC	AGC	CCA	GAC	AGC	CCG	GGC	ATC	CCC	GAA	AGG	3330
S	P	R	W	P	E	G	A	C	R	Q	P	G	A	L	Q	G	E	M	S	1130
TCC	CCC	CGC	TGG	CCT	GAG	GGT	GCC	TGC	AGG	CAA	CCG	GGG	GCC	CTG	CAG	GGA	GAG	ATG	AGT	3390
A	L	F	A	Q	K	L	E	E	I	R	S	K	S	P	M	F	S	A	G	1150
GCC	TTG	TTT	GCT	CAA	AAG	CTG	GAG	GAG	ATC	AGG	AGT	AAA	TCC	CCC	ATG	TTC	TCC	GCC	GGT	3450
K	P	L	L	P	C	V	V	L	P	H	A	P	G	M	A	G	P	G	S	1170
AAG	CCC	CTC	TTG	CCC	TGC	GTG	GTC	CTC	CCG	CAC	GCC	CCT	GGC	ATG	GCT	GGG	CCT	GGG	TCA	3510
P	A	A	A	S	A	W	T	V	S	P	R	V	L	V	L	V	A	L	Y	1190
CCT	GCT	GCT	GCT	TCT	GCG	TGG	ACG	GTG	TCG	CCT	CGT	GTG	CTC	GTG	CTC	GTG	GCT	CTG	TAT	3570
P	W	H	C	L	R	G	T	L	L	P	W	L	A	C	G	P	*			1208
CCG	TGG	CAC	TGT	CTC	CGT	GGC	ACT	CTG	CTC	CCT	TGG	CTT	GCC	TGT	GGC	CCA	TAG			3624

←SEQ ID NO:3↑

CCCCAGCCCTCCTGTCTGAGCTTGAGGCCCTGGGACTTGGGTGGAGCTGGTTTGAGGCCCGACAGGCTGGGAAGAACCA
GCTGCTCTTGTCTGAGGGTCTGGGGCCGGGACTGTGGCCTGACATGTGGGCCCTCCGGCTGGGCGCTTCCCCAAACTC
ACCTCCTGGGCGGCTGGCGACCTGCATGGCCCTGATGCCCTTCTCTGGGACTGGGGGCCATGTACCATCCCATTTCCAC
CTCCCTCTAGGGCAGGCTCCAGGGGTCCCTACTGGGAAGTCTGATGTGGGCAGGTAGTGCAGCTGCTGGGCGTCTCCTG
CGCCCCCTGGGACGCTGGAGCCTGCTGAGTGCTGCGTGGAGTAGATTCCCTGGGCCCCAGGGCTTCGCTGCTTTGGGCT
GAAGCACCCTACTAGAAGGGTGTCTCCTTAGCCTGGAGGGAGGGACATACACGGAGCCCGCCCCACACCACCTGCCCC
TCCAGACCCCTGACCAAGCTTTCCTTTCTGCCCCACCCACGCTTGCCTCCGTAGTTAGGAAGTGAAGCGGCGAGT
GACAGGTAACGGGGCCAGCCCCG

FIGURE 1c

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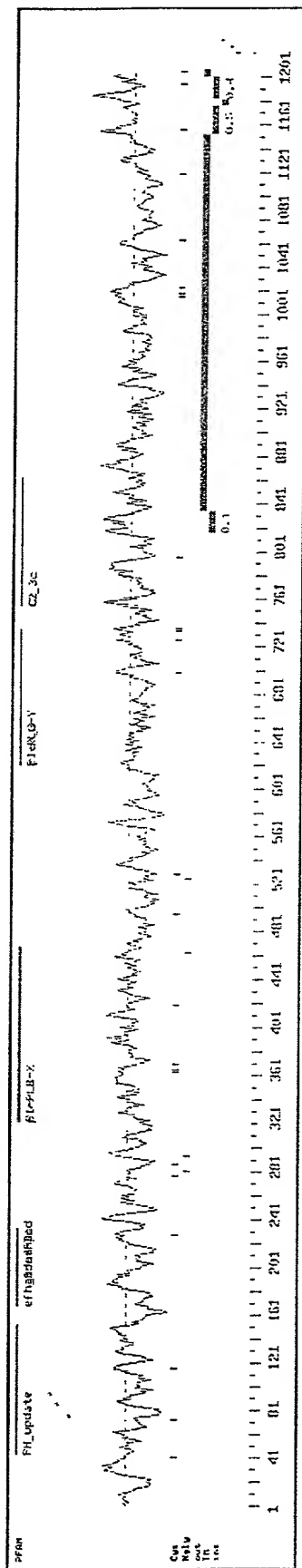


Fig. 2

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32544 44 *->vikeGwLlks...kswkkRyfvLfn..nvLlyykdskkkpkgsipL SEQ ID NO:4
+ eG ++k +++++ R+ L +++++ + ++ k+ k +i++
AMQEGMQMVKLrggSKGLVRFYLLDEhrSCIRWRPSR-KNEKAKISI 89
sgc.qvek.pd.....kncFeirt.dr..tlllqaeseeer
+++++v ++ ++ ++ +++++ +++++CF i ++++++l l +s+e +
32544 90 DSIqEVSEgRQsevfqrypdsfdpNCCFSIYHgSHreSLDLVSTSSEVA 139
keWvkaiqsair<-*
++Wv+ ++++++
32544 140 RTWVTGLRYLMA 151

Fig. 3

32544 169 *->elkeaFkefDkDgDGkIsfeEfkaalkkl<-* SEQ ID NO:5
lk+ F+e+Dk+gDG +s+ E +++l+k1
WLKQTFDEADKNGDGSLSIGEVLLHKL 197

Fig. 4a

32544 205 *->elkeaFkefDk.DgDGkIsfeEfkaalkkl<-* SEQ ID NO:6
++k++F+e+D++D+ G++ feEf+a+ k++
RVKQMFREADTdDHQGTlGFEEFCaFYKMM 234

Fig. 4b

32544 323 *->dmsiPLsHYfisSshntYLTgkQlwGkssvesYrqQLdaGcRcvELD SEQ ID NO:7
dm +PLsHYfi+SshntYL g+Ql ++s v +Y +L+aGcRcvE D
DMTQPLSHYFITSSHNTYLVGDLMSQSRVDMYAWVLQAGCRCVEVD 369
cwdGkpddepiIyHGhtltleiklkdVleaIkdfafkPtSpyPvIlSlEn
cwdG pd+epi+ HG+tlT++i++kdV+e+I ++af +yPvIlS+en
32544 370 CWDG-PDGEPIVHHGYTLTSKILFKDVIETINKYAFI-KNEYPVILSIEN 417
HcnsddqQrkmakyfkeiFgdmLltkPtldslttepglpLPslkdIrgKI
Hc++ qQ+kma+y+ +i+gd+L + + +t+ LPs+ +l+gKI
32544 418 HCSVI-QQKMAQYLTdILGDkLDLSSVSSEDATT----LPSPQMLKGKI 462
LLknkk<-*
L+k+kk
32544 463 LVKGKK 468

Fig. 5

FIG. 3

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*->ElsnLvnYiqsikFrsFelsGeekntsyeisSFsErkvkakllkes SEQ ID NO:8
ls+Lv Y +s+ ++ e s ++sSFsE+ ka + l++
32544 621 ALSDLVKYTKSV--ATHDIE-MEAASSWQVSSFSET--KAHQILQOK 662

pvefVkyNkrqLsRvYPkGtRvDSSNfmPqvFWnaGCQmVALNfQTSdIp
p + ++N+ qLsR+YP RvDSSN++Pq+fWnaGCQmVALN+Q+ +
32544 663 PAQYLRFNQQQLSRIYPSSYRVDSSNYPQPFWNAGCQmVALNYQSEGRM 712

mqiNdGmFeyNggqPdGsfsGYlLKPeFlR<-*
+q+N ++F++Ngg +GY+LKP ++
32544 713 LQLNRAKFSANGG-----CGYVLKPGCMC 736
```

Fig. 6

```
*->LtVtvieArnLpkmDk....vngrlsDPYVkvslldkdkkfkT SEQ ID NO:9
L+ ++i++++Lpk + + ++ ++ ++DP+V+v+++g+++d ++ +T
32544 756 LVLRIISGQQLPKPRDsmldRGE-IIDPFVEVEIIGLPVDCSREQT 801

kvvktNGLNPvWneEtFvFekvplpelasktLrfaVyDedrfsrddfiG
+vv ++ G+NP+W Et+vF v++pe+a +rf V+D+d ++ DfiG
32544 802 RVVDDN-GFNPTWE-ETLVFM-VHMPEIAL--VRFLVWDHDPiG-RDFiG 845

qvt<-*
q+t
32544 846 QRT 848
```

Fig. 7

Query: 883 KVKQALGLKGLFLRGPKPGSLDASHAAGRPPARPSVSQRILRRTASAPTKSQKPGRRGFPE 942
+VKQALGLKGLFLRGPKPGSLDASHAAGRPPARPSVSQRILRRTASAPTKSQKPGRRGFPE
Sbjct: 101 QVKQALGLKGLFLRGPKPGSLDASHAAGRPPARPSVSQRILRRTASAPTKSQKPGRRGFPE 160 SEQ ID NO:10

Query: 943 LVLGTRDTGSKXXXXXXXXXXXXXXXXXXXXXXXXXSGSPRGKAPAAVAEKSPVRVRPPRV 1002
LVLGTRDTGSK SSGSPRGKAPAAVAEKSPVRVRPPRV
Sbjct: 161 LVLGTRDTGSKGVADDVPPGPGPAPEAPAQEGPGSGSPRGKAPAAVAEKSPVRVRPPRV 220

Query: 1003 LDGPGPAGMAATCMKCVVGSCAGVNTGGLQRRERPPSPGPASXXXXXXXXXXXXDSLGA 1062
LDGPGPAGMAATCMKCVVGSCAGVNTGGLQRRERPPSPGPAS DSLGA
Sbjct: 221 LDGPGPAGMAATCMKCVVGSCAGVNTGGLQRRERPPSPGPASQAIRQPRARADSLGA 280

Query: 1063 CCGLDPHAIPGRSREAPKPGAWRQXXXXXXXXXXXXXXXXXXXXIPERSPRWPEGACRQ 1122
CCGLDPHAIPGRSREAPKPGAWRQ IPERSPRWPEGACRQ
Sbjct: 281 CCGLDPHAIPGRSREAPKPGAWRQPGGSGSMSSDSSSPDIPERSPRWPEGACRQ 340

Query: 1123 GALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPHXXXXXXXXXXXXXWTVSPR 1182
GALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPH WTVSPR
Sbjct: 341 GALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPHAPGMAGPGSPAAASAWTVSPR 400

Query: 1183 VLVLVALYPWHCLRGTLPLWLACGP 1207
VLVLVALYPWHCLRGTLPLWLACGP
Sbjct: 401 VLVLVALYPWHCLRGTLPLWLACGP 425

Fig. 8

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Query: 307 SPAGDIFNPEHHHVHQM TQPLSHYFITSSHNTYL VGDQLMS-QSRVDMYAWVLQAGCRC 365
SP ++F+PEH VHQM QPLSHYFI SSHNTYL G+QL S +S V+MY L GCRC
Sbjct: 2 SPDCNVFDP EHKQVHQM NQPLSHYFINSSHNTYL TGNQLSSGESSVEMYRQALLKGCRC 61 SEQ ID NO:11

Query: 366 VEVDCWDGPDG--EPIVHHGYTLT SKILFKDVIETINKYAFIKNEYPVILSIENHCSVI- 422
+E+DCWDG DG EPI+ HG+T+T++I PKD +E I ++AF+ +EYPVILS+ENHC
Sbjct: 62 IELDCWDGKGDPEPIITHGHTMTTEISFKDCLEAIKEHAFVTSEYPVILSLENHCDSTP 121

Query: 423 -QQKKMAQYLT DILGDKL---DLSSVSSEDATTLPS PQ 456
QQ KMA+Y ++ GD L L E LPSP+
Sbjct: 122 QQQAKMAEYCKEVFGDMLFTEPLEESPLEPGKELPSPE 159

Fig. 9a

Query: 514 KRKLD SLIKESKIRDCEDPNNFSVSTLSPSGKLGRKSKAEEDVESGEDA 562
KRK+ LIK K+++ + S K +++EE+ E G DA
Sbjct: 162 KRKI--LIK NKKLKEHSEEKE-----SEEKKTDEETES EEEDEMGSDA 202 SEQ ID NO:12

Fig. 9b

Query: 742 PNSEDPLPGQLKKQLVLR 759
P E P P +LK+++++
Sbjct: 151 PGKELPSPEELKRKILIK 168 SEQ ID NO:13

Fig. 9c

Query: 41 CMGAMQEGMQMVKL RGGSKGLVRFYYLDEHRSCIRWRP---SRKN-EKAKISIDSIQEV S 96
C+ MQ+G ++ K+R S R++ LD+ + W P S+K+ EK K I I+E+
Sbjct: 14 CLQFMQKGSELKKVRSNSWKYNRYFTLDDDMQTLWWEPHWFSSKKDSEKPKFDISDIKEIR 73 SEQ ID NO:14

Query: 97 EGRQSEVFQRYPDGSF---DP-NCCFSIYHGSH--RESLDLVSTSSEVARTWVTGLRYLM 150
G+ +E F R F +P +CCFSI G + ESLDLV+ S++VA WV+GLRYL+
Sbjct: 74 MGKNTETF-RNNGKEFQIQEPEDCCFSIIFGENYFHESLDLVANSADVANIWVSGRLRYLV 132

Query: 151 AGISDEDSLARRQRT RDQWLKQTFDEADKNGDGSLSIGEV LQLLHKLVNVLPRQRVKQMF 210
+ L Q DQWL++ F +AD+N D +S E LL +NV + + +F
Sbjct: 133 DYA--KHMLDNYQEQLDQWLREWFQQADRNKDSRMSFREAQNLLKLMNVQMDEEYAFSIF 190

Query: 211 READ 214
RE D
Sbjct: 191 RECD 194

Fig. 10

32544-03100
T00T00"2T23660

Title: 32544, A NOVEL HUMAN PHOSPHOLIPASE C AND
USES THEREOF

Inventors: Rachel Meyers et al.

Application No.: Not yet assigned

Docket No.: 381552004800

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Query: 174 FDEADKNGDGSLSIGEVLLQLLHKLNVNLPQRVKQMFREAD--TDDHQGT-LGFEEFCAF 230
FDE D +G+G L + + LN L ++ F+E + + + T + E F
Sbjct: 2 FDEFDTDGNGHLDEQTAFKCIKHLNPRLKHHKITNKFKEITIKSKEKERTKITKEHFVDL 61 SEQ ID NO:15

Query: 231 YKMMSTRDLYLLMLTYSNKHDLDAASLQRFLOVEQKMAGVTLESCQDIIEQFEPCPEN 290
YK + TR ++Y LM+ YS +KD+LD L FL+ EQ M VT ++C DIIEQ+EPC E
Sbjct: 62 YKELGTRPEVYFLMVQYSKNKYLDLDCQDLMLFLETEQGMVHVTEDNCLDIIEQYEPCEG 121

Query: 291 KSKGLLGIDGFTNY 304
+ G + IDGFT+Y
Sbjct: 122 RENGWMTIDGFTSY 135

Fig. 11

Query: 851 FSSMMPGYRHHVYLEGMEEASIFVHVAVSDISGKVKQALGLKGLFLRGPKPGSLDASHAAGR 910
FSS++PGYRHHVYLEG+ EASIFVH+ +++I GK +Q GLKGLF + P+ S ++++
Sbjct: 2 FSSLVPGYRHHVYLEGLETEASIFVHITINEIYGKNRQLQGLKGLFNKNPRHSSSENNS--H 59 SEQ ID NO:16

Query: 911 PPARPSVSQRILRRTASAPTKSQKPGRRGFPELV 944
+ S+ RILRRTASAP K +K + GF E+V
Sbjct: 60 YVRKRSIGDRILRRTASAPAKGRKKS KMGFQEMV 93

Fig. 12

FOOTED " 2122660